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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re U.S. Patent Application of)
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KAMBARA *at al.*)
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Application Number: 10/083,340)
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Filed: February 27, 2002)
)
For: METHOD FOR TESTING)
NUCLEIC ACID SEQUENCE)
)
Attorney Docket No. ASAM.0055)

Honorable Assistant Commissioner
for Patents
Washington, D.C. 20231

RESPONSE AND AMENDMENT UNDER 37 C.F.R. §1.111

Sir:

This is in response to the **Notice to File Missing Parts** dated March 22, 2002, the period for response to which is to expire on MAY 22, 2002. Applicants hereby submit the shortened abstract, the nucleotide and/or amino acid sequence listing and the statement concurrently.

IN THE ABSTRACT

Please replace the Abstract of the Disclosure currently on file with the following substitute Abstract:

> A method for examining nucleotide sequences of a sample includes adding a group of primers of multiple species to a solution containing the sample and simultaneously synthesizing complementary strands at each of the multiple regions containing the nucleotide sequences; designing the DNA probes with specific sequences elongate the complementary strands by the presence or absence of mutations in the nucleotide sequences, wherein the same number of such DNA probes and the nucleotide sequences are used for complementary strand synthesis; using the nucleotide sequences or their complementary sequences as a template to convert pyrophosphate produced during the elongation reaction to ATP which then reacts with chemiluminescent substrates to develop luminescence to be detected. According to the method, sensitivity is greatly increased by amplification of the amount of pyrophosphate produced in synthesis of the complementary strands without amplifying the copies of nucleotide sequences.

REMARKS

The above resubmission along with the following remarks are being submitted as a full and complete response to the **Notice to File Missing Parts** dated March 22, 2002, the period for response to which will expire on May 22, 2001. The listing was composed via PatentIN 3.0 software and checked via Checker 3.0 software which showed no errors. The Examiner is respectfully requested to review the application and to indicate the allowability of the claims.

Substantive consideration of the application and its claims is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

Respectfully submitted,

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SPF/JCM/JT

Marked-up Version of Amended Abstract

[An effective] A method for examining nucleotide sequences of a sample [having multiple test sites based on a method using chemiluminescence, which comprises a step in which] includes adding a group of primers [1 consisting] of multiple [primer] species [is added] to a solution containing [a] the sample [2 subjected to examination,] and simultaneously synthesizing [synthesis of] complementary strands [is performed] at each of the multiple regions containing [target] the nucleotide sequences [to be examined]; [a step in which] designing the DNA probes with specific sequences [are designed so that elongation of] elongate the complementary strands [is affected] by the presence or absence of mutations in the [target] nucleotide sequences, wherein the same number of such DNA probes and the [target]nucleotide sequences [is] are used for complementary strand synthesis[, 5-1 and 5-2]; [a step in which the elongation reaction of complementary strands] using the [targets] nucleotide sequences or [the sequence] their complementary sequences [to the targets] as a template to convert [and the following reaction where] pyrophosphate produced during the elongation reaction [is converted] to ATP [and reacted] which then reacts with chemiluminescent substrates to develop luminescence to be detected[are performed in the subcells of the reaction vessel that are compartmentalized for each target; wherein a step in which mutations present in the target nucleotide sequences are detected by detecting the luminescence]. According to the method, sensitivity is greatly increased by amplification of the amount of pyrophosphate produced in synthesis of the complementary strands without amplifying the [copy number of targets] copies of nucleotide sequences.